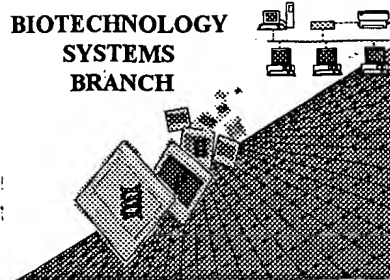


0570
12/7

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/821,782
Source: 01PE
Date Processed by STIC: 12/17/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by the treatment given to all mail coming via the Brentwood Mail Facility.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)

2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202

3. Hand Carry directly to:

U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
1911 South Clark Street, Crystal Mall One, Sequence Information, Arlington, VA 22202

Or

U.S. Patent and Trademark Office, 2011 South Clark Place, Customer Window, Box Sequence, Crystal Plaza Two,
Lobby, Room 1B03, Arlington, Virginia 22202

4. Federal Express Delivery, 2011 South Clark Street, Crystal Plaza 2, Room 1B03-Mailroom, Box Sequence,
Arlington, VA 22202

ERROR DETECTED**SUGGESTED CORRECTION**SERIAL NUMBER: 09/821,782

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFT

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequences. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) . . .
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/821,782

DATE: 12/17/2001
TIME: 15:11:29

pg 1-7

Input Set : A:\821782seq.oct.txt
Output Set: N:\CRF3\12172001\I821782.raw

Does Not Comply
Corrected Diskette Needed

4 <110> APPLICANT: Kumar Verma, Sunil
5 Singh, Lalji
7 <120> TITLE OF INVENTION: UNIVERSAL PRIMERS FOR WILDLIFE IDENTIFICATION
9 <130> FILE REFERENCE: U-013365-9
11 <140> CURRENT APPLICATION NUMBER: 09/821782
13 <141> CURRENT FILING DATE: 2001-03-29
15 <160> NUMBER OF SEQ ID NOS: 255

ERRORED SEQUENCES

17 <210> SEQ ID NO: 1
19 <211> LENGTH: (25) 26 *shown*
21 <212> TYPE: DNA
23 <213> ORGANISM: Artificial Sequence
25 <220> FEATURE:
27 <223> OTHER INFORMATION: Universal primer "mcb 398" for amplifying fragment of
cytochrome b gene
28 of animal species
30 <400> SEQUENCE: 1
E--> 32 taccatgagg acaaatatcta ttctg (25) 26
411 <210> SEQ ID NO: 19
413 <211> LENGTH: (328) 327
415 <212> TYPE: DNA
417 <213> ORGANISM: gz21CL
419 <220> FEATURE:
421 <223> OTHER INFORMATION: DNA sequence generated from the known clouded leopard
(Neofelis
422 nebulosa) animal number 1 using primers mcb398 and mcb869
424 <400> SEQUENCE: 19
426 tgaatctgag gaggcttctc agtagacaaa gccaccctga cagcattttt cgccttccac
427 ttcatcctcc catttatcat ctgagcctta gcagcagttc accttctatt tctccatgaa
E--> 428 aaggatcca ataaccctc aggaatggtta tccgattcag acaaaatccc gttccaccgc
E--> 429 tactatacaa tcaaagatat cctaggcctc ctagtcttaa ttctagcgt cactactatt
E--> 430 gttctattct cccagacct actaggagac cctgacaatt acactccgc caaccctcta
E--> 431 aataccctc cccatatcaa gcctgaat
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436 <211> LENGTH: (328) 327
438 <212> TYPE: DNA
440 <213> ORGANISM: gz22CL
442 <220> FEATURE:
444 <223> OTHER INFORMATION: DNA sequence generated from the known clouded leopard
(Neofelis
445 nebulosa) animal number 2 using primers mcb398 and mcb869
447 <400> SEQUENCE: 20
449 tgaatctgag gaggcttctc agtagacaaa gccaccctga cagcattttt cgccttccac
450 ttcatcctcc catttatcat ctgagcctta gcagcagttc accttctatt tctccatgaa
E--> 451 aaggatcca ataaccctc aggaatggtta tccgattcag acaaaatccc gttccaccgc

(25) 26

60
120
(180) 179
240
300
328
nos. off
due to
above error

60
120
(180) 179

see pg 2-3

E--> 452 tactatacaa tcaaagatat cctaggcctc ctagttctaa ttctagecgt cacactactt
E--> 453 gttctattct ccccagacct actaggagac cctgacaatt acactcccgc caaccctcta

240
300 nos.
off

RAW SEQUENCE LISTING

DATE: 12/17/2001

PATENT APPLICATION: US/09/821,782

TIME: 15:11:29

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Output Set: N:\CRF3\12172001\I821782.raw

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 961 <211> LENGTH: 472
 963 <212> TYPE: DNA
 965 <213> ORGANISM: Redunca fulvorufula
 967 <400> SEQUENCE: 45
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 970 tcccatacat cggcacaarc ctagttagaat gaatctgagg aggrtttctca gtggataaag 120
 971 caaccctcac tcgattcttc gccttcact ttatcctccc atttatcatc atagccctcg 180
 972 ctatagtcca cctactattc ctccatgaaa caggatccaa caaccccaca ggggtttcat 240
 E--> 973 cagayatgga caaatccca ttccaccct actacacat caaagayatt ctagggtccc 300
 974 tactactaat cctggccctt acactattag tactattcac cctgaccta ctgggagacc 360
 975 cggacaatta caccagca aaccactca acacacccc tcacatcaa ccagaatggt 420
 E--> 976 atttcttatt ngcatagca atcctacgat caatcccaa taaactagga gg 472
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 1240 <211> LENGTH: 472
 1242 <212> TYPE: DNA
 1244 <213> ORGANISM: Balaenoptera bonaerensis
 1246 <400> SEQUENCE: 59
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 1249 tcccatacat tggtagacc ttagttagaat gaatctgagg tggcttctct gtagacaaaag 120
 1250 caacattaac acgctttttt gccttcact tcattctccc ttctattatc ctatgattag 180
 1251 caattgtcca cctcattttt ctccgcaaaa caggatccaa taaccccaca ggtattccat 240
 1252 ctgatataga caaatccca ttccaccctt attacacaa caaagacatt ctaggcgccc 300
 1253 tactactaat tctaacccta ctaaacactaa ccctattcgc acccgacctg ctgggagacc 360
 1254 ccgacaacta caccagca aaccactca gtacccagc acacattaaa ccagaatgat 420
 E--> 1255 attttctatt cgcatacga atcctacgat caatcccaa taaactaggc gg 472
 1257 <211> LENGTH: 472
 1259 <212> TYPE: DNA
 1261 <213> ORGANISM: Balaenoptera borealis
 W--> 1263 <210> SEQ ID NO:
 E--> 1263 <400> SEQUENCE: 60
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 1266 tcccatacat tggtagacc ctagttagaat ggatctgagg cggtttctct gtagataaag 120
 1267 caacactaac acgctttttt gccttcact tcattctccc ctctattatt ctatgactag 180
 1268 caatggtcca cctcattttt ctccatgaaa caggatccaa caaccccaca ggtattccat 240
 1269 ccgacataga caaatccca ttccaccctt actacacagt taaagacatt ctaggcgccc 300
 1270 tactactaat cctaacccta ctaataactaa ccctattcgc acccgacctg ctgggagacc 360
 1271 cagacaacta caccagca aatccactca gtacccagc acacattaaa ccagaatgat 420
 E--> 1272 atttcttatt tgcatacga atcctacgat caatcccaa caaattaggc gg 472
 E--> 1275 <210> SEQ ID NO: 61
 1277 <211> LENGTH: 472
 1279 <212> TYPE: DNA
 1281 <213> ORGANISM: Balaenoptera edeni
 E--> 1283 <400> SEQUENCE: (60) 61 ← please edit
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 1286 tcccatacat tggtagacc ctagttagaat gaatctggg cggtttctct gtagataaag 120
 1287 caacactaac acgctttttt gccttcact ttatcctccc ctctattatt ctatgactag 180
 1288 caatggtcca cctcattttt ctccacgaaa caggatccaa taaccccaca ggtattccat 240

328

numbering
offsee
item 9on
Even
summary
sheetdelete
hard page
break(hard page
breaks are
not
permitted
in
computer
readable
form)

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/821,782

DATE: 12/17/2001

TIME: 15:11:29

Input Set : A:\821782seq.oct.txt

Output Set: N:\CRF3\12172001\I821782.raw

1289 ccaacataga caaaatccca ttccaccctt attacacaac taaagacatt ctaggcgccc 300
 1290 tactactaat cctaacccta ctaatgctaa ccctattcgt acccgacctt cttggagacc 360
 1291 cagacaacta cactccagca aatccactca gtaccccaac acacattaaa ccagaatgat 420
 1292 atttcctatt tgcatacgca atcctacgat caattcccaa caaattaggc gg 472
 2304 <210> SEQ ID NO: 13 *113 ← change*
 2306 <211> LENGTH: 472
 2308 <212> TYPE: DNA
 2310 <213> ORGANISM: Hyperoodon ampullatus
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 2314 taccctgagg acaaatatca ttctgaggcg caaccgtcat caccaatctc ctatccgcca 60
 2315 ttccctatat cggcactacc ctagttaga gaactgagg tggtttctcc gtagacaaag 120
 2316 ccacattaac ccgctttttc gccctccact ttatctctcc attcattatt ctagccctag 180
 2317 caatcgctca cctactattc ctccatgaaa caggatccaa caatcccaca ggaattccat 240
 2318 ctgacataga caaaatcccg ttccacccat actacacaa caagacact ctaggggccc 300
 2319 tattactaat cctagtctca ctacacattaa ccctattcgc acccgacctt ctaggagacc 360
 2320 ctgataacta taccacagca aacccactca gcaactcagc acacatcaaa ccagaatggt 420
 2321 acttcttatt tgcatacgca atcctacggt caatccctaa caaactagga gg 472
EX -> 2324 <210> SEQ ID NO: 114
 3404 <210> SEQ ID NO: 169
 3406 <211> LENGTH: 472
 3408 <212> TYPE: DNA
 3410 <213> ORGANISM: Afropavo congensis
 3412 <400> SEQUENCE: 169
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 3415 tccctatat tggtaaaacc ctagttaga ggcctgagg aggattotca gttgacaacc 120
 3416 caaccctcac ccgattcttc gccctacact ttcttctccc ctttctaatt gcgggaatta 180
 3417 caattatcca cctcacattc ctccatgaat caggctcaaa caaccactg ggcattctcat 240
 3418 ccaattcaga taaaatccca ttccaccgt actactccct caagatatc ctaggcttag 300
 3419 cactcatgct cattccattc ctgacactag ccctactctc cccaacctc ttaggtgatc 360
 3420 cagaaaactt caccacagca aaccctctag taactcccc acacattaaa ccagaatggt 420
 E--> 3421
 atttcttatt tgcctatgcc atccttcgct caatcccaaa caaactagga gg 472
 3423 <211> LENGTH: 472
 3425 <212> TYPE: DNA
 3427 <213> ORGANISM: Pavo muticus
EX -> 3429 <210> SEQ ID NO:
EX -> 3429 <400> SEQUENCE: 170
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 3432 tccctatat tggacaaacc ctagttaga gagcctgagg ggcattctca gtcgacaacc 120
 3433 caaccctcac ccgattcttc gccctacact ttctctctcc ctttgtaatc gcaggaatta 180
 3434 caattatcca cctcacattc ctccatgaat caggctcaaa taatccacta ggcattctcat 240
 3435 ccaactcaga caaaattccg ttccacccat actactccct caagatatc ctaggcttaa 300
 3436 ctcttatatt tatccattc ctaacactag ccctattctc cccaatctc ctaggtgacc 360
 3437 cagaaaactt taccacagca aaccctctag taaccccc gcacattaaa ccagaatgat 420
EX -> 3438 atttcttatt tgcctacgcc atccttcggt caatcccaaa caaactagga gg 472
EX -> 3441 <210> SEQ ID NO: 171
 4283 <210> SEQ ID NO: 214
 4285 <211> LENGTH: 23 *22 (p.5)*
 4287 <212> TYPE: DNA
 4289 <213> ORGANISM: Artificial Sequence

472<210> 170

delete hard
 page break code

RAW SEQUENCE LISTING

DATE: 12/17/2001

PATENT APPLICATION: US/09/821,782

TIME: 15:11:29

Input Set : A:\821782seq.oct.txt

Output Set: N:\CRF3\12172001\I821782.raw

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4291 <220> FEATURE:
4293 <223> OTHER INFORMATION: Primer for amplifying a fragment of cytochrome b
4294     gene of animal species in polymerase chain reaction
4296 <400> SEQUENCE: 214
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4301 <210> SEQ ID NO: 215
4303 <211> LENGTH: (23) 22
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4307 <213> ORGANISM: Artificial Sequence
4309 <220> FEATURE:
4311 <223> OTHER INFORMATION: Primer for amplifying a fragment of cytochrome b
4312     gene of animal species in polymerase chain reaction
4314 <400> SEQUENCE: 215
E--> 4316 atgcaaata ggaagtatca ttc                                22
4319 <210> SEQ ID NO: 216
4321 <211> LENGTH: 472
4323 <212> TYPE: DNA
4325 <213> ORGANISM: Aepyceros melampus
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E--> 4331 caacccttac cgcatttttc gcyttccact tcatcyttcc attcatcatt gcggcactag      180
4332 ccatagtcca cctactcttt ctccacgaaa caggatctaa caaccctaca ggaatcttat      240
4333 cagattcaga taaaattcca ttccaccctt actatactat traagacatc ctaggaatcc      300
4334 tattaataat tctagtccta atactcctag tactattcat acccgaccta ctaggagacc      360
E--> 4335 cagacaanna catcccgca aaccactca acaccctcc ccacatcaag cccgaatggt      420
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4342 <212> TYPE: DNA
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4350 caacccttac cgcattcttt gcctttcact tcatctttcc atttatcatc gcagccctag      180
4351 ccatagtaca cctactcttt ctccacgaaa cagggtccaa taaccccaca ggaatctcat      240
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4353 tattactaat tctagcttta ttactcttag tattattcac acctgacctt cttggagacc      360
4354 cagataacta caccacagca aaccactca aactccccc tcacattaaa ccagaatggt      420
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4524 <213> ORGANISM: Bison bonasus
4526 <400> SEQUENCE: 226
4528 taccatgagg acaaatatca ttttgaggag caacagtcac taccaacctc ctatcagcaa      60
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4530 caacccttac cgcatttttc gctttccact ttatctctcc atttattatc atagcaattg      180
4531 ccatagttca cctactattc ctccacgaaa caggttctaa caatccaaca ggaatttcct      240

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see Item 9 on Eva
summary
sheet

Item 9

P. 6

RAW SEQUENCE LISTING

DATE: 12/17/2001

PATENT APPLICATION: US/09/821,782

TIME: 15:11:29

Input Set : A:\821782seq.oct.txt

Output Set: N:\CRF3\12172001\I821782.raw

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4534 cagataacta caccacagca aatccactta acacacctcc ccacatcaaa cccgaatgat 420
E--> 4535 acttcttatt tgcatangca attttacggg caatcccca caaactagga gg item 9 472
4794 <210> SEQ ID NO: 240
4796 <211> LENGTH: 472
4798 <212> TYPE: DNA
4800 <213> ORGANISM: Rupicapra rupicapra
4802 <400> SEQUENCE: 240
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4805 tcccgatatat tggcacagac ttagtcgaat gaatctgagg aggccttctc gtagacaagg 120
4806 ctaccctcac ccgattcttt gccttccact tcactctccc atttatcatt gcagccttag 180
4807 ccctagtcca cctactcttc ctccacgaaa caggatctaa caaccacaca ggaatcccat 240
E--> 4808 cagatgcgga caaaatccca tttnacccct attataccat caaagacatt ctgggcgcca 300
E--> 4809 tactactaat cctcaccctc atactactag tactattnac acctgacctc ctcgagagacc 360 item 9
4810 cagataatta caccacagcg aaccactca acacaccccc tcacattaaa cccgagtgat 420
4811 atttcttatt tgcatatgca attctacgat caatcccca caaacttgga gg 472
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4879 <213> ORGANISM: Ovis vignei
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4886 ctatagtcca cctactcttc ctccacgaaa caggatccaa taaccacaca ggaattccat 240
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4888 tcctactaat cctcatcctc atgctgctag tactattcac gcctgactta cttggagacc 360
4889 cagacaacta caccacagca aaccacttta acactcccc tcacatcaaa cctgaatgat 420
4890 atttcctatt tgcatatgca atcttacgat caatccctaa taaactagga gg 472
5089 <210> SEQ ID NO: 255
5091 <211> LENGTH: 472
5093 <212> TYPE: DNA
5095 <213> ORGANISM: Cervus elaphus canadensis
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5101 caaccctaac ccgattcttc gctttccact ttattctccc atttatcatc gcagcactcg 180
5102 ctatagtaca cttactcttc cttcacgaga caggatctaa taaccaaca ggaatcccat 240
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5104 tacttctaata actcttcccta atattactag tattattcgc accagatctg cttggagacc 360
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see next page

09/21, 782

7

<210> 255

<211> 472

<212> DNA

<213> Cervus elaphus canadensis

~~L2207~~

<400> AB021096 → L2237

move up to L2237 line

L4007 always has the sequence ID number as a response

L4007 255

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/821,782

DATE: 12/17/2001

TIME: 15:11:31

Input Set : A:\821782seq.oct.txt

Output Set: N:\CRF3\12172001\I821782.raw

L:32 M:254 E: No. of Bases conflict, LENGTH:Input:25 Counted:26 SEQ:1
 L:32 M:252 E: No. of Seq. differs, <211>LENGTH:Input:25 Found:26 SEQ:1
 L:428 M:254 E: No. of Bases conflict, LENGTH:Input:180 Counted:179 SEQ:19
 M:254 Repeated in SeqNo=19
 L:431 M:252 E: No. of Seq. differs, <211>LENGTH:Input:328 Found:327 SEQ:19
 L:451 M:254 E: No. of Bases conflict, LENGTH:Input:180 Counted:179 SEQ:20
 M:254 Repeated in SeqNo=20
 L:454 M:252 E: No. of Seq. differs, <211>LENGTH:Input:328 Found:327 SEQ:20
 L:973 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:45
 M:340 Repeated in SeqNo=45
 L:1255 M:254 E: No. of Bases conflict, LENGTH:Input:60 Counted:474 SEQ:59
 L:1255 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:8
 L:1255 M:252 E: No. of Seq. differs, <211>LENGTH:Input:472 Found:474 SEQ:59
 L:1263 M:282 W: Numeric Field Identifier Missing, <210> is required.
 L:1263 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:59 differs:60
 L:1275 M:214 E: (33) Seq.# missing, SEQ ID NO:60
 L:1283 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:61 differs:60
 L:2312 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:13 differs:113
 L:2324 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 14 thru 113
 L:3421 M:254 E: No. of Bases conflict, LENGTH:Input:170 Counted:474 SEQ:169
 L:3421 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:8
 L:3421 M:252 E: No. of Seq. differs, <211>LENGTH:Input:472 Found:474 SEQ:169
 L:3429 M:282 W: Numeric Field Identifier Missing, <210> is required.
 L:3429 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:169 differs:170
 L:3441 M:214 E: (33) Seq.# missing, SEQ ID NO:170
 L:4298 M:252 E: No. of Seq. differs, <211>LENGTH:Input:23 Found:22 SEQ:214
 L:4316 M:252 E: No. of Seq. differs, <211>LENGTH:Input:23 Found:22 SEQ:215
 L:4330 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:216
 M:340 Repeated in SeqNo=216
 L:4355 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:217
 L:4535 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:226
 L:4808 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:240
 M:340 Repeated in SeqNo=240
 L:4887 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:244
 L:5097 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:255 differs:254